

04CD
04/10/2004
OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/808,898

DATE: 04/02/2001
TIME: 10:54:56

Input Set : A:\128seq.001
Output Set: N:\CRF3\04022001\I808898.raw

3 <110> APPLICANT: Bryan, Bruce
4 Szent-Gyorgyi, Christopher
5 Szczepaniak, William
8 <120> TITLE OF INVENTION: RENILLA RENIFORMIS FLOURESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
9 FLOURESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH THROUGHPUT
10 SCREENING AND NOVELTY ITEMS
12 <130> FILE REFERENCE: 24729-128
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/808,898
C--> 15 <141> CURRENT FILING DATE: 2001-03-15
17 <150> PRIOR APPLICATION NUMBER: 60/189,691
18 <151> PRIOR FILING DATE: 2000-03-15
20 <150> PRIOR APPLICATION NUMBER: 09/277,716
21 <151> PRIOR FILING DATE: 1999-03-26
23 <150> PRIOR APPLICATION NUMBER: 08/757,046
24 <151> PRIOR FILING DATE: 1996-11-25
26 <150> PRIOR APPLICATION NUMBER: 08/597,274
27 <151> PRIOR FILING DATE: 1996-02-06
29 <150> PRIOR APPLICATION NUMBER: 08/908,909
30 <151> PRIOR FILING DATE: 1997-08-08
32 <150> PRIOR APPLICATION NUMBER: 08/990,103
33 <151> PRIOR FILING DATE: 1997-12-12
35 <160> NUMBER OF SEQ ID NOS: 33
37 <170> SOFTWARE: FastSEQ for Windows Version 4.0
39 <210> SEQ ID NO: 1
40 <211> LENGTH: 1196
41 <212> TYPE: DNA
42 <213> ORGANISM: Renilla reniformis
44 <220> FEATURE:
45 <221> NAME/KEY: CDS
46 <222> LOCATION: (1)...(942)
47 <223> OTHER INFORMATION: Renilla reniformas luciferase
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52 1 5 10 15
54 atg ata act ggt ccg cag tgg tgg gcc aga tgt aaa caa atg aat gtt 96
55 Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
56 20 25 30
58 ctt gat tca ttt att aat tat tat gat tca gaa aaa cat gca gaa aat 144
59 Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
60 35 40 45
62 gct gtt att ttt tta cat ggt aac gcg gcc tct tct tat tta tgg cga 192
63 Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
64 50 55 60
66 cat gtt gtg cca cat att gag cca gta gcg cgg tgt att ata cca gat 240
67 His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
68 65 70 75 80

ENTERED

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70 ctt att ggt atg ggc aaa tca ggc aaa tct ggt aat ggt tct tat agg      288
71 Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
72                               85                               90                               95
74 tta ctt gat cat tac aaa tat ctt act gca tgg ttg aac ttc tta att      336
75 Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
76                               100                               105                               110
78 tac caa aga aga tca ttt ttt gtc ggc cat gat tgg ggt gct tgt ttg      384
79 Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
80                               115                               120                               125
82 gca ttt cat tat agc tat gag cat caa gat aag atc aaa gca ata gtt      432
83 Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
84                               130                               135                               140
86 cac gct gaa agt gta gta gat gtg att gaa tca tgg gat gaa tgg cct      480
87 His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
88 145                               150                               155                               160
90 gat att gaa gaa gat att gcg ttg atc aaa tct gaa gaa gga gaa aaa      528
91 Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
92                               165                               170                               175
94 atg gtt ttg gag aat aac ttc ttc gtg gaa acc atg ttg cca tca aaa      576
95 Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
96                               180                               185                               190
98 atc atg aga aag tta gaa cca gaa gaa ttt gca gca tat ctt gaa cca      624
99 Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
100                               195                               200                               205
102 ttc aaa gag aaa ggt gaa gtt cgt cgt cca aca tta tca tgg cct cgt      672
103 Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
104                               210                               215                               220
106 gaa atc ccg tta gta aaa ggt ggt aaa cct gac gtt gta caa att gtt      720
107 Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
108 225                               230                               235                               240
110 agg aat tat aat gct tat cta cgt gca agt gat gat tta cca aaa atg      768
111 Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
112                               245                               250                               255
114 ttt att gaa tcg gat cca gga ttc ttt tcc aat gct att gtt gaa ggc      816
115 Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
116                               260                               265                               270
118 gcc aag aag ttt cct aat act gaa ttt gtc aaa gta aaa ggt ctt cat      864
119 Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
120                               275                               280                               285
122 ttt tcg caa gaa gat gca cct gat gaa atg gga aaa tat atc aaa tcg      912
123 Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
124                               290                               295                               300
126 ttc gtt gag cga gtt ctc aaa aat gaa caa taattacttt gggtttttat      962
127 Phe Val Glu Arg Val Leu Lys Asn Glu Gln
128 305                               310
130 ttacattttt cccgggttta ataataaaa tgtcattttc aacaatttta ttttaactga      1022
131 atattttcaca gggaacattc atatatgttg attaatntag ctogaacttt actctgtcat      1082
132 atcatttttg aatattacct ctttcaatga aactttataa acagtgggtc aattaattaa      1142
133 tatatattat aattacattt gttatgtaat aaactcgggt ttattataaa aaaa      1196

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137 <210> SEQ ID NO: 2
138 <211> LENGTH: 1822
139 <212> TYPE: DNA
140 <213> ORGANISM: Cypridina hilagendorfii luciferase
142 <220> FEATURE:
143 <221> NAME/KEY: CDS
144 <222> LOCATION: (1)...(1665)
145 <223> OTHER INFORMATION: Cypridina hilgendorfii luciferase
147 <400> SEQUENCE: 2
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150 1 5 10 15
152 aac tgc cag gat gca tgt cct gta gaa gct gaa gca ccg tca agt aca      96
153 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
154 20 25 30
156 cca aca gtc cca aca tct tgt gaa gct aaa gaa gga gaa tgt atc gat      144
157 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
158 35 40 45
160 acc aga tgc gca aca tgt aaa cga gac ata cta tca gac gga ctg tgt      192
161 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
162 50 55 60
164 gaa aat aaa cca ggg aag aca tgc tgt aga atg tgc cag tat gta att      240
165 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
166 65 70 75 80
168 gaa tcc aga gta gaa gct gct gga tat ttt aga acg ttt tac gcc aaa      288
169 Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys
170 85 90 95
172 aga ttt aat ttt cag gaa cct ggt aaa tat gtg ctg gct cga gga acc      336
173 Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
174 100 105 110
176 aag ggt ggc gac tgg tct gta acc ctc acc atg gag aat cta gat gga      384
177 Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
178 115 120 125
180 cag aag gga gct gta ctg act aag aca aca ctg gag gta gta gga gac      432
181 Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp
182 130 135 140
184 gta ata gac att act caa gct act gca gat cct atc aca gtt aac gga      480
185 Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
186 145 150 155 160
188 gga gct gac cca gtt atc gct aac ccg ttc aca att ggt gag gtg acc      528
189 Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
190 165 170 175
192 att gct gtt gtc gaa ata ccc ggc ttc aat att aca gtc atc gaa ttc      576
193 Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
194 180 185 190
196 ttt aaa cta atc gtg ata gat att ctg gga gga aga tct gtg aga att      624
197 Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
198 195 200 205
200 gct cca gac aca gca aac aaa gga ctg ata tct ggt atc tgt ggt aat      672

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201	Ala	Pro	Asp	Thr	Ala	Asn	Lys	Gly	Leu	Ile	Ser	Gly	Ile	Cys	Gly	Asn	
202		210				215						220					
204	ctg	gag	atg	aat	gac	gct	gat	gac	ttt	act	aca	gac	gca	gat	cag	ctg	720
205	Leu	Glu	Met	Asn	Asp	Ala	Asp	Asp	Phe	Thr	Thr	Asp	Ala	Asp	Gln	Leu	
206	225					230						235				240	
208	gcg	atc	caa	ccc	aac	ata	aac	aaa	gag	ttc	gac	ggc	tgc	cca	ttc	tac	768
209	Ala	Ile	Gln	Pro	Asn	Ile	Asn	Lys	Glu	Phe	Asp	Gly	Cys	Pro	Phe	Tyr	
210					245					250					255		
212	ggg	aat	cct	tct	gat	atc	gaa	tac	tgc	aaa	ggg	ctc	atg	gag	cca	tac	816
213	Gly	Asn	Pro	Ser	Asp	Ile	Glu	Tyr	Cys	Lys	Gly	Leu	Met	Glu	Pro	Tyr	
214				260					265					270			
216	aga	gct	gta	tgt	cgt	aac	aat	atc	aac	ttc	tac	tat	tac	act	ctg	tcc	864
217	Arg	Ala	Val	Cys	Arg	Asn	Asn	Ile	Asn	Phe	Tyr	Tyr	Tyr	Thr	Leu	Ser	
218		275						280						285			
220	tgc	gcc	ttc	gct	tac	tgt	atg	gga	gga	gaa	gaa	aga	gct	aaa	cac	gtc	912
221	Cys	Ala	Phe	Ala	Tyr	Cys	Met	Gly	Gly	Glu	Arg	Ala	Lys	His	Val		
222		290				295						300					
224	ctt	ttc	gac	tat	gtt	gag	aca	tgc	gct	gca	ccg	gaa	acg	aga	gga	acg	960
225	Leu	Phe	Asp	Tyr	Val	Glu	Thr	Cys	Ala	Ala	Pro	Glu	Thr	Arg	Gly	Thr	
226	305				310						315					320	
228	tgt	gtt	tta	tca	gga	cat	act	ttc	tat	gac	aca	ttc	gac	aaa	gcc	aga	1008
229	Cys	Val	Leu	Ser	Gly	His	Thr	Phe	Tyr	Asp	Thr	Phe	Asp	Lys	Ala	Arg	
230				325					330					335			
232	tat	caa	ttc	cag	ggc	cca	tgc	aaa	gag	ctt	ctg	atg	gcc	gca	gac	tgt	1056
233	Tyr	Gln	Phe	Gln	Gly	Pro	Cys	Lys	Glu	Leu	Leu	Met	Ala	Ala	Asp	Cys	
234				340					345					350			
236	tac	tgg	aac	aca	tgg	gat	gta	aag	gtt	tca	cat	aga	gat	gtt	gag	tca	1104
237	Tyr	Trp	Asn	Thr	Trp	Asp	Val	Lys	Val	Ser	His	Arg	Asp	Val	Glu	Ser	
238		355						360						365			
240	tac	act	gag	gta	gag	aaa	gta	aca	atc	agg	aaa	cag	tca	act	gta	gta	1152
241	Tyr	Thr	Glu	Val	Glu	Lys	Val	Thr	Ile	Arg	Lys	Gln	Ser	Thr	Val	Val	
242		370				375						380					
244	gat	ttg	att	gtg	gat	ggc	aag	cag	gtc	aag	gtt	gga	gga	gtg	gat	gta	1200
245	Asp	Leu	Ile	Val	Asp	Gly	Lys	Gln	Val	Lys	Val	Gly	Gly	Val	Asp	Val	
246	385					390					395					400	
248	tct	atc	ccg	tac	agt	tct	gag	aac	aca	tcc	ata	tac	tgg	cag	gat	gga	1248
249	Ser	Ile	Pro	Tyr	Ser	Ser	Glu	Asn	Thr	Ser	Ile	Tyr	Trp	Gln	Asp	Gly	
250				405						410					415		
252	gac	atc	ctg	acg	acg	gcc	atc	cta	cct	gaa	gct	ctt	gtc	gtt	aag	ttc	1296
253	Asp	Ile	Leu	Thr	Thr	Ala	Ile	Leu	Pro	Glu	Ala	Leu	Val	Val	Lys	Phe	
254				420					425					430			
256	aac	ttt	aag	cag	ctc	ctt	gta	gtt	cat	atc	aga	gat	cca	ttc	gat	gga	1344
257	Asn	Phe	Lys	Gln	Leu	Leu	Val	Val	His	Ile	Arg	Asp	Pro	Phe	Asp	Gly	
258		435						440						445			
260	aag	aca	tgc	ggc	ata	tgt	ggg	aac	tat	aat	caa	gat	tca	act	gat	gat	1392
261	Lys	Thr	Cys	Gly	Ile	Cys	Gly	Asn	Tyr	Asn	Gln	Asp	Ser	Thr	Asp	Asp	
262		450					455					460					
264	ttc	ttt	gac	gca	gaa	gga	gca	tgc	gct	ctg	acc	ccc	aat	ccc	cca	gga	1440
265	Phe	Phe	Asp	Ala	Glu	Gly	Ala	Cys	Ala	Leu	Thr	Pro	Asn	Pro	Pro	Gly	

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266 465          470          475          480
268 tgt aca gag gag cag aaa cca gaa gct gag cga ctc tgc aat agt cta      1488
269 Cys Thr Glu Glu Gln Lys Pro Glu Ala Glu Arg Leu Cys Asn Ser Leu
270          485          490          495
272 ttt gat agt tct atc gac gag aaa tgt aat gtc tgc tac aag cct gac      1536
273 Phe Asp Ser Ser Ile Asp Glu Lys Cys Asn Val Cys Tyr Lys Pro Asp
274          500          505          510
276 cgt att gca cga tgt atg tac gag tat tgc ctg agg gga cag caa gga      1584
277 Arg Ile Ala Arg Cys Met Tyr Glu Tyr Cys Leu Arg Gly Gln Gln Gly
278          515          520          525
280 ttc tgt gac cat gct tgg gag ttc aaa aaa gaa tgc tac ata aag cat      1632
281 Phe Cys Asp His Ala Trp Glu Phe Lys Lys Glu Cys Tyr Ile Lys His
282          530          535          540
284 gga gac act cta gaa gta cca cct gaa tgc caa' taaatgaaca aagatacaga      1685
285 Gly Asp Thr Leu Glu Val Pro Pro Glu Cys Gln
286 545          550          555
288 agctaagact actacagcag aagataaaag agaagctgta gttcttcaaa aacagtatat      1745
289 tttgatgtac tcattgttta cttacataaa aataaattgt tattatcata acgtaaagaa      1805
290 aaaaaaaaaa aaaaaaa      1822
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 1644
295 <212> TYPE: DNA
296 <213> ORGANISM: Luciola cruciata
298 <220> FEATURE:
299 <221> NAME/KEY: CDS
300 <222> LOCATION: (1)...(1644)
301 <223> OTHER INFORMATION: Luciola cruciata luciferase
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306 1          5          10          15
308 ttt tac cct atc gaa gag gga tct gct gga aca caa tta cgc aaa tac      96
309 Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Thr Gln Leu Arg Lys Tyr
310          20          25          30
312 atg gag cga tat gca aaa ctt ggc gca att gct ttt aca aat gca gtt      144
313 Met Glu Arg Tyr Ala Lys Leu Gln Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
314          35          40          45
316 act ggt gtt gat tat tct tac gcc gaa tac ttg gag aaa tca tgt tgt      192
317 Thr Gly Val Asp Tyr Ser Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
318          50          55          60
320 cta gga aaa gct ttg caa aat tat ggt ttg gtt gtt gat ggc aga att      240
321 Leu Gly Lys Ala Leu Gln Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
322 65          70          75          80
324 gcg tta tgc agt gaa aac tgt gaa gaa ttt ttt att cct gta ata gcc      288
325 Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Ile Ala
326          85          90          95
328 gga ctg ttt ata ggt gta ggt gtt gca ccc act aat gag att tac act      336
329 Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
330          100          105          110

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VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date